

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: MAERTENS, GEERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
- (ii) TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
ISOLATES
- (iii) NUMBER OF SEQUENCES: 97
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BIERMAN & MUSERLIAN
(B) STREET: 600 THIRD AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10016
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/256,568
(B) FILING DATE: 18-JUL-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP93/03325
(B) FILING DATE: 26-NOV-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP/93/402,129.6
(B) FILING DATE: 31-AUG-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP/92/403,222.0
(B) FILING DATE: 27-NOV-1992
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: CHARLES A. MUSERLIAN
(B) REGISTRATION NUMBER: 19,683
(C) REFERENCE/DOCKET NUMBER: 410.004
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 661-8000
(B) TELEFAX: (212) 661-8002

099930.0000

27

(C) INDIVIDUAL ISOLATE: HCV (Okamoto et al., 1991)

(A) CHROMOSOME/SEGMENT: HCV

(ix) FEATURE:

(B) LOCATION: 1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

21

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV

(A) CHROMOSOME/SEGMENT: HCV

(B) MAP POSITION: Position -264 of 5' end

(ix) FEATURE:

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /standard_name=
"Universal HCV primer HcPr95"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

26

(2) INFORMATION FOR SEO ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV

(B) MAP POSITION: Position -29 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /standard_name=
"Universal HCV primer HcPr96"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CACTCGCAAG CACCCTATCA GGCAGT

26

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 1 (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 1

(B) MAP POSITION: position -170 of the 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 1 specific Probe HcPr124"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTGCCAGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 1 (Kato et al., 1990)
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV type 1
 - (B) MAP POSITION: position -117 of 5'end
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /standard_name= "HCV type 1 specific Probe HcPr125"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCTCCAGGCA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA

09859302.070601

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 1b (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 1b

(B) MAP POSITION: position -103 of the 5'end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 1b specific Probe HcPr138"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCGCGAGACT GCTAGC

16

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 2

(B) MAP POSITION: position -83 of the 5'end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 2 specific Probe HcPr147"

T09070"20E66660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TAGCGTTGGG TTGCGA

16

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2a (Chan et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 2a
- (B) MAP POSITION: position -168 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2a specific probe HcPr136"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTRCCGGRAA GACTGG

16

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

099070-20566850

16

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 2b (Nakao et al., 1991)
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV type 2b
 - (B) MAP POSITION: position -117 of 5' end
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /standard_name= "HCV type 2b specific probe HcPr127"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGACCGGACA TAGAGT

16

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 3
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV type 3
 - (B) MAP POSITION: position -170 of 5' end

109070.20E66666

(D) OTHER INFORMATION: /standard_name= "HCV type
3 specific probe HcPr128"

16

(D) TOPOLOGY: linear

(D) OTHER INFORMATION: /standard_name= "HCV type
3 specific probe HcPr 129"

16

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 3a (Chan et al., 1992)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 3a

(B) MAP POSITION: position -146 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type
3a specific probe HcPr140"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCTTGGAGCA ACCCGC

16

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 3b (Chan et al., 1992)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 3b

(B) MAP POSITION: position -146 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type
3b specific probe HcPr139"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TCTTGGAACA ACCCGC

16

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 4 (Bukh et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 4
- (B) MAP POSITION: position -170 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 4 specific probe HcPr 144"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AATYGCCGGG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

099070-20666660

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 4

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 4

(B) MAP POSITION: position -147 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 4 specific probe HcPr145"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTCTTGGAAC TAACCC

16

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 4

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 4

(B) MAP POSITION: position -117 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 4 specific probe HcPr146"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTCCGGGCA TTGAGC

16

0969302.070604

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1990)
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV
 - (B) MAP POSITION: position -115 of 5' end
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /standard_name="Universal HCV probe HcPr 142"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGGGCGYGC CCCC GC

16

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 3
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV type 3
 - (B) MAP POSITION: position -103 of 5' end

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..16
 (D) OTHER INFORMATION: /standard_name= "HCV type
 3 specific probe HcPr 154"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CCGCGAGATC ACTAGC

16

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: HCV type 2a (Okamoto et
 al., 1991)

- (viii) POSITION IN GENOME:
 (A) CHROMOSOME/SEGMENT: HCV type 2a
 (B) MAP POSITION: position -165 of 5' end

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..16
 (D) OTHER INFORMATION: /standard_name= "HCV type
 2a specific probe HcPr156"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CCGGGAAGAC TGGGTC

16

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

09869302.07001

(iii) ANTI-SENSE: NO

(C) INDIVIDUAL ISOLATE: HCV type 2b (Okamoto et al., 1992)

(A) CHROMOSOME/SEGMENT: HCV type 2b

(ix) FEATURE:

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type
2b specific probe HcPr157"

CCGGAAAGAC TGGGTC

16

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2a (Okamoto et al., 1991)

(A) CHROMOSOME/SEGMENT: HCV type 2a

(B) MAP POSITION: position -136 of 5' end

(A) NAME/KEY: misc feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type
2a specific probe HcPr158"

ACCCACTCTA TGCCCG

16

(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

(C) INDIVIDUAL ISOLATE: HCV type 2b (Okamoto et al., 1992)

(B) MAP POSITION: position -136 of 5' end

(D) OTHER INFORMATION: /standard_name= "HCV type
2b specific probe HcPr159"

ACCCACTCTA TGTCCG

16

(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2 (Okamoto et al., 1992)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 2

(B) MAP POSITION: position -126 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 2 specific probe HcPr160"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATAGAGTGCG TTTATC

16

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV

(B) MAP POSITION: Position -195 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "Universal HCV probe HcPr153"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TCTGCGGAAC CGGTGA

16

0999'0" 20E66960

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AATTGCCAGG AYGACC

16

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GCTCAGTGCC TGGAGA

16

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

09899300-070601

CCGCGAGACY GCTAGC

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCCCGCAAGA CTGCTA

16

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CGTACAGCCT CCAGGC

16

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGACCCAGTC TTCCTG

16

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TGCCTGGTCA TTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TKTCTGGGTA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

TO9070"20E66860

16

16

16

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GAGTGTTGTG CAGCCT

16

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AATCGCCGGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

0959306-00601

AATGCCCGGC AATTG

16

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

AATCGCCGAG ATGACC

16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

AATGCTCGGA AATTG

16

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) ANTI-SENSE: NO

GAGTGTCGAA CAGCCT

16

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AATTGCCGGG ATGACC

16

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

TCTCCGGGCA TTGAGC

16

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

16

(D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

16

(D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

16

(2) INFORMATION FOR SEQ ID NO: 50:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:
```

TGCCTGGAAA TTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 51:

- ```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 16 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

GAGTGTCGTA CAGCCT

16

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AGTYCACCGG AATCGC

16

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGAATCGCCA GGACGA

16

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAATCGCCGG GTTGAC

16

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

0999002066660

(vii) IMMEDIATE SOURCE:

(B) CLONE: jp62

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GAGTGTCGTA CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG	120
CCCGGCCATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGCGTTGG GTTGCGA	177

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb81

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GAGTGTCGTA CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG	120
CCCGGTCATT TGGGCGTGCC CCCGCAAGAC CGCTAGCCGA	160
GTAGCGTTGG GTTGCGA	177

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid

0909070"20E66660

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: br56

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAGTGTCTGTG CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA	120
CCCAGAAATT TGGGCGTGCC CCCGCGAGAT CACTAGCCGA	160
GTAGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: bu79

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5'untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GAGTGTTGTA CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGACGACC GGGTCCTTTC TTGGATTAAAC CCGCTCAATG	120
CCCGGAAATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA	160
GTAGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: bu74

- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GAGTGTGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTCCA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGAATAA CCCGCTCAAT	120
GCCCGGAAAT TTGGGCGTGC CCCC GCGAGA CTGCTAGCCG	160
AGTAGTGTG GTCGCGA	178

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: gb80

- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GAGTGTCGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGAATAA CCCGCTCAAT	120

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(2) INFORMATION FOR SEQ ID NO: 61:

- (ii) MOLECULE TYPE: cDNA

- (viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GAGTGTCTGTG	CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTACA	CCGGAATTGC	80
CAGGACGACC	GGGTCTTTT	TTGGATCAAC	CCGCTCAATG	120
CCTGGAGATT	TGGGCGTGCC	CCCGCGAGAC	CGCTAGCCGA	160
GTAGTGTGG	GTCGCGA			177

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
(B) CLONE: be90

- (viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GAGTGTCGTG CAGCCTCCAG GATCCCCCCT CCCGGGAGAG 40

CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 80
CAGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAGTG 120
CCTGGAGATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA 160
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: be91

(viii) POSITION IN GENOME:
 (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GAGTGTCGTA CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG 40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 80
CGGAAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG 120
TCCGGTCATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCTA 160
GTAGCGTTGG GTTGCGA 177

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: be92

099900.0000
T09070.20E6660

- (viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GAGTGTCTGTA CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CAGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG	120
CCTGGTCATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGCGTTGG GTTGCGA	177

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: be93

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAGTGTCTGTG CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA	120
CCCAGACATT TGGGCGTGCC CCCGCGAGAT CACTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

0989302-07004

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: be94

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGTGTCTGTG CAGCCTCCAG GGGGGGGCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA	120
CCCAGACATT TGGGCGTGCC CCCGCAAGAT CACTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb48

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GAGTGTTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG	120
CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

099930-0000

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb116

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GAGTGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb569

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAGTGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG	120

0999303-070601

CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA 160
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb358

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG 40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC 80
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG 120
CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA 160
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb549

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

GAGTGTTGTG	CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTTCA	CCGGAATCGC	80
CGGGACGACC	GGGTCCTTTC	TTGGAACAAA	CCCCTCAAT	120
GCCCGGCAAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	160
AGTAGTGTTG	GGTCGCGA			178

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: cam600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GAGTGTGTA	CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTACA	CCGGAATCGC	80
CGAGATGACC	GGGTCTTTC	TTGGATCAAC	CCGCTCAATG	120
CTCGGAAATT	TGGGCGTGCC	CCCGCAAGAC	TGCTAGCCGA	160
GTAGTGTGG	GTCGCGA			177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

GAGTGTGTA	CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTACA	CCGGAATCGC	80
CGAGATGACC	GGGTCCTTTC	TTGGATCAAC	CCGCTCAATG	120
CTCGGAAATT	TGGGCGTGCC	CCCGCAAGAC	TGCTAGCCGA	160
GTAGTGTG	GTCGCGA			177

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: qb809

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

GAGTGTGTGTA	CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTACA	CCGGAATCGC	80
CGAGATGACC	GGGTCCTTTC	TTGGATCAAC	CCGCTCAATG	120
CTCGGAAATT	TGGGCGTGCC	CCCGCAAGAC	CGCTAGCCGA	160
GTAGTGTGG	GTCGCGA			177

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb487

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CAGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb724

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GAGTGTCGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTTCA CCGGAATCGC	80
CAGGACGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: be97

(viii) POSITION IN GENOME:
 (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GAGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CAGGACGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: be95

(viii) POSITION IN GENOME:
 (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GAGTGTCGAA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CGGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120

1099300-07001

CCCGGAGATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA 160
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: be96
- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: 5' untranslated region
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

GAGTGTCGAA CAGCCTCCAG GACCCCCCT CCCGGGAGAG 40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 80
CGGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG 120
CCCGGAGATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA 160
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: be98
- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GAGTGTCTGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGTTGACC GGGTCCTTTC TTGGAAC TAC CCGCTCAATG	120
CCCGGAAATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA	160
GTAGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb438

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GAGTGTCGAA CAGCCTCCAG GATCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTTCA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGAATCAA CCCGCTCAAT	120
GCCCGGAAAT TTGGGCGTGC CCCC GCGAGA CTGCTAGCCG	160
AGTAGTGTTG GGTCGCGA	178

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1099070-2025550

(vii) IMMEDIATE SOURCE:

(B) CLONE: be90

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu
1          5          10
Ser Ile Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala
15          20
Arg Gln Ala Ile Lys Ser Leu Thr Glu Arg Leu Tyr
25          30          35
Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu
50          55          60
Thr Thr Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu
65          70
Lys Ala Ser Ala Ala Cys Arg Ala Ala Lys Leu Gln
75          80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85          90          95
Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala
100          105
Ala Ser Leu Arg Val
110

```

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: be91

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu
1          5          10
Ser Ile Tyr Gln Ala Cys Ser Leu Pro Gln Glu Ala
15          20

```

Arg Thr Val Ile His Ser Leu Thr Glu Arg Leu Tyr
 25 30 35
 Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser
 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe
 50 55 60
 Thr Thr Ser Met Gly Asn Thr Met Thr Cys Tyr Ile
 65 70
 Lys Ala Leu Ala Ala Cys Lys Ala Ala Gly Ile Val
 75 80
 Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu
 100 105
 Arg Asn Leu Arg Ala
 110

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be92

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu
 1 5 10
 Ser Ile Tyr Leu Ala Cys Ser Leu Pro Glu Gln Ala
 15 20
 Arg Thr Ala Ile His Ser Leu Thr Glu Arg Leu Tyr
 25 30 35
 Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln Thr
 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe
 50 55 60
 Thr Thr Ser Met Gly Asn Thr Ile Thr Cys Tyr Val
 65 70
 Lys Ala Gln Ala Ala Cys Lys Ala Ala Gly Ile Ile
 75 80
 Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

09899300100601

Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu
 100 105
 Arg Asn Leu Arg Ala
 110

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be93

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu
 1 5 10
 Glu Ile Tyr Gln Cys Cys Asn Leu Glu Pro Glu Ala
 15 20
 Arg Lys Val Ile Ser Ser Leu Thr Glu Arg Leu Tyr
 25 30 35
 Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln
 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu
 50 55 60
 Pro Thr Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile
 65 70
 Lys Ala Thr Thr Ala Ala Lys Ala Ala Gly Leu Arg
 75 80
 Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg
 100 105
 Ala Ala Leu Arg Ala
 110

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

099970-2056550

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb48

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1          5          10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
          15          20
Arg Lys Ala Ile Thr Ala Leu Thr Glu Arg Leu Tyr
25          30          35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
          40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50          55          60
Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
          65          70
Lys Ala Ser Ala Ala Ile Lys Ala Ala Gly Leu Arg
75          80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85          90          95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys
          100          105
Arg Pro Leu Gly Ala
110

```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb116

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1          5          10

```

0939302-070604

Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
 15 20
 Arg Arg Ala Ile Thr Ala Leu Thr Glu Arg Leu Tyr
 25 30 35
 Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu
 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
 50 55 60
 Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
 65 70
 Lys Ala Ser Ala Ala Ile Arg Ala Ala Gly Leu Arg
 75 80
 Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys
 100 105
 Arg Ala Leu Gly Ala
 110

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb215

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
 1 5 10
 Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
 15 20
 Arg Lys Val Ile Thr Ala Leu Thr Glu Arg Leu Tyr
 25 30 35
 Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
 50 55 60
 Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
 65 70
 Lys Ala Ser Ala Ala Ile Arg Ala Ser Gly Leu Arg
 75 80

109970-2055550

(2) INFORMATION FOR SEQ ID NO: 89:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

(2) INFORMATION FOR SEQ ID NO: 90:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb549

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu											
1				5					10													
Glu	Ile	Tyr	Gln	Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala											
		15					20															
Arg	Lys	Val	Ile	Ser	Ala	Leu	Thr	Glu	Arg	Leu	Tyr											
25					30					35												
Val	Gly	Gly	Pro	Met	Tyr	Asn	Ser	Lys	Gly	Asp	Leu											
			40				45															
Cys	Gly	Gln	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr											
	50					55				60												
Thr	Thr	Ser	Phe	Gly	Asn	Thr	Val	Thr	Cys	Tyr	Leu											
			65						70													
Lys	Ala	Val	Ala	Ala	Thr	Arg	Ala	Ala	Gly	Leu	Lys											
		75				80																
Gly	Cys	Ser	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val											
85					90					95												
Val	Ile	Cys	Glu	Ser	Gly	Gly	Val	Glu	Glu	Asp	Ala											
			100					105														
Arg	Ala	Leu	Arg	Ala																		
			110																			

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: gb809

1099070-20E56850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu
1           5           10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15           20
Arg Lys Val Ile Ala Ala Leu Thr Glu Arg Leu Tyr
25           30           35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
40           45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50           55           60
Thr Thr Ser Phe Gly Asn Thr Met Thr Cys Tyr Leu
65           70
Lys Ala Ser Ala Ala Ile Arg Ala Ala Gly Leu Lys
75           80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85           90           95
Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys
100          105
Arg Ala Leu Gly Ala
110

```

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be95

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu
1           5           10
Ser Ile Tyr Gln Ser Cys Asp Leu Gln Pro Glu Ala
15           20
Arg Ala Ala Ile Arg Ser Leu Thr Gln Arg Leu Tyr
25           30           35
Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
40           45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe
50           55           60

```

09993002-070601

Thr Thr Ser Met Gly Asn Thr Met Thr Cys Tyr Ile
65 70
Lys Ala Leu Ala Ser Cys Arg Ala Ala Arg Leu Arg
75 80
Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu
100 105
Ala Ser Leu Arg Ala
110

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GAGTGTGTGTA CAGCCTCC

18

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

TGCCCCGGA AAA TTTGGGC

17

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

TGCCCCGGAGA TTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GAGTGTGGAA CAGCCTC

17

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GGGGGCCTGG AGGCTG

16

Variable	Mean	SD	Min	Max
Age	30.5	4.2	18	45
Gender	1.2	0.4	1	2
Education	12.5	1.5	9	16
Marital status	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Family size	1.5	0.5	1	2
Urban/rural	1.5	0.5	1	2
Religious affiliation	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Income	1.5	0.5	1	2
Health status	1.5	0.5		